IN THE SPECIFICATION:

Please replace the paragraph at page 4, line 19 with the following amended paragraph:

There has been much interest in protein-protein interactions in the field of proteomics. A number of biochemical approaches have been used to identify interacting proteins. These approaches generally employ the affinities between interacting proteins to isolate proteins in a bound state. Examples of such methods include coimmunoprecipitation and copurification, optionally combined with cross-linking to stabilize the binding. Identities of the isolated protein interacting partners can be characterized by, e.g., mass spectrometry. *See e.g.,* Rout *et al., J. Cell. Biol.,* 148:635-651 (2000); Houry *et al., Nature,* 402:147-154 (1999); Winter *et al., Curr. Biol.,* 7:517-529 (1997). A popular approach useful in large-scale screening is the phage display method, in which filamentous bacteriophage particles are made by recombinant DNA technologies to express a peptide or protein of interest fused to a capsid or coat protein of the bacteriophage. A whole library of peptides or proteins of interest can be expressed and a bait protein can be used to ~~screening~~ screen the library to identify peptides or proteins capable of binding to the bait protein. *See e.g.,* U.S. Patent Nos. 5,223,409; 5,403,484; 5,571,698; and 5,837,500. Notably, the phage display method only identifies those proteins capable of interacting in an *in vitro* environment, while the coimmunoprecipitation and copurification methods are not amenable to high throughput screening.